

protein	localization	pH-optimum	pH-ave	pH_best	pH-stab_average	pH_ave	pH_best	delta-intervals	pl	molecular weight	temp	Reference
Candidapepsin from <i>Candida pulcherrima</i>	extracellular	2.5-3.5	3	3.5	3--5	4	3.5	0	4.7	36500		1
thiosulfate dehydrogenase from <i>Acidithiobacillus t</i>	periplasm	3.5	3.5	3.5	5--7	6	5	-1.5	8.9			2
beta-galactosidase from <i>Oryza sativa</i>	extracellular	3.5	3.5	3.5	5	5	5	-1.5				3
beta-glucuronidase from <i>Aspergillus niger</i>	Cellwall	3	3	3	2--9	4.5	3	0				4
beta-galactosidase from <i>Guehomyces pullulans</i>	extracellular	4.5	4.5	4.5	4--7	5.5	4.5	0				5
adenosine nucleosidase from <i>Camellia sinensis</i>		4	4	4	6--8	7	6	-2		67000	60	NA
alpha-N-arabinofuranosidase from <i>Aspergillus niger</i>		4	4	4	4 -- 7	5.5	4	0	3.5	47000		6
tripeptidyl-peptidase I from <i>Rattus norvegicus</i>		4	4	4	5--6	5.5	5	-1				7
xylan 1,4-beta-xylosidase from <i>Penicillium wortman</i>	extracellular	3.3-4.0	3.65	4	5.0-6.0	5.5	5	-1	5	31000		8
protein-glutamate methyl esterase from <i>Rattus norve</i>		4	4	4	2--10	6	4	0	4.45			9
.pyranose oxidase from <i>Trametes multicolor</i>	intracellular	4	4	4	5--7	6	4	-1				10
fructan beta-fructosidase from <i>Penicillium sp.</i>	extracellular	4.5	4.5	4.5	4--10	7	4.5	0				11
Mucorpepsin from <i>Mucor pusillus</i>	intracellular	3.7 --3.8 prot C/ 3.5--3.6 prot D	3.7	3.8	4 prot c / 5 prot d	4.5	4	-0.2			44	12
protein-tyrosine-phosphatase from <i>Periplaneta amer</i>	vesicles	4	4	4	(up to 5)						25	13
fructose 5-dehydrogenase from <i>Gluconobacter indust</i>		4	4	4	4.5 --6	5.25	4.5	-0.5			60	14
xylan 1,4-beta-xylosidase from <i>Aspergillus oryzae</i>		4	4	4	3 --7	5	4	0				15
polygalacturonase from <i>Cryptococcus albidus</i>	extracellular	3.75	3.75	3.75	4 -- 8	6	4	-0.25	8.1		60	16
alpha-galactosidase from <i>Trichoderma reesei</i>	extracellular	4	4	4	4 -- 8	6	4	0	5.2		40	17
alpha-glucuronidase from <i>Aspergillus niger</i>		3.0-3.5	3.25	3.15	2.0-4.5	3.15	3.15	0		150000	50	18
beta-N-acetylhexosaminidase from <i>Trichoderma harzi</i>		4.0-5.5	4.75	5.5	3--9	6	5.5	0				19
3-phosphoglycerate phosphatase from <i>Spinacia olera</i>		5.8	5.8	5.8	5.8--7.0	6.9	5.8	0			65	20
glucan 1,4-alpha-glucosidase from <i>Chaetomium therm</i>		4	4	4	3.5-8 (max at 3.5)	3.5	4	0			50	21
feruloyl esterase from <i>Aspergillus niger</i>		5	5	5	4-9.5	6.25	5	0			45	22
polygalacturonase from <i>Rhizopus oryzae</i>	extracellular	4.5	4.5	4.5							60	23
beta-fructofuranosidase from <i>Candida utilis</i>	periplasm	5.5	5.5	5.5	3.0-6.0	4.5	5.5	0				24
alpha-N-acetylglucosaminidase from <i>Homo sapiens</i>	lysosome	4.5	4.5	4.5	6.5-8.5	7.5	6.5	-2	5.1	29000		25
gamma-glutamyl hydrolase from <i>Sus scrofa</i>		4.0-4.5	4.25	4.5	7	7	7	-2.5	8.5		60	26
3-phytase from <i>Pantoea agglomerans</i>		4.5	4.5	4.5								27
beta-N-acetylhexosaminidase from <i>Sclerotinia fruct</i>	extracellular	4.4	4.4	4.4	4--11	7.5	4.4	0				28
beta-mannosidase from <i>Homo sapiens</i>		4.5	4.5	4.5					4.7			29
cathepsin D from <i>Bos taurus</i>		4.2	4.2	4.2	5--7	6	5	0			55	30
fructan beta-fructosidase from <i>Alternaria alternat</i>	extrallular	4.5	4.5	4.5	4--5	4.5	4.5	0		102000		31
cellobiose dehydrogenase (acceptor) from <i>Schizophy</i>	Exracellular				4--11	7.5	7.5			250000	60	32
beta-galactosidase from <i>Rhizomucor sp.</i>	extracellular	4.5	4.5	4.5	3.5-7.5	5.5	4.5	0	4.2			33
Aspergillopepsin I from <i>Aspergillus oryzae</i>	membrane	4.5	4.5	4.5	3--6	4.5	4.5	0				34
beta-glucosidase from <i>Thermoascus aurantiacus</i>		5	5	5	3--8	5	5	0			40	35
alpha,alpha-trehalase from <i>Saccharomyces cerevisiae</i>		5	5	5						430	30	36
beta-fructofuranosidase from <i>Aureobasidium pullula</i>		5	5	5	6 -- 11	8.5	6	-1			55	37
3-phytase from <i>Aspergillus niger</i>		5	5	5								38
glucan 1,4-alpha-glucosidase from <i>Aspergillus nige</i>		4.8	4.8	4.8	2 -- 7	4.5	4.8	0			17	39
nitric-oxide reductase from <i>Pseudomonas stutzeri</i>		4.8	4.8	4.8							43	40
manganese peroxidase from <i>Bjerkandera adusta</i>		5	5	5					3.55		43	41
glutaryl-7-aminocephalosporanic-acid acylase from		5.5	5.5	5.5	4 --10	7	5.5	0	5.3			42
hyaluronan synthase from <i>Streptococcus equisimilis</i>		9--10	9.5	9	6.5--11	8.75	9	0			55	43
glucan endo-1,3-beta-D-glucosidase I from <i>Hordeum</i>		4.8	4.8	4.8							40	44
glucan endo-1,3-beta-D-glucosidase II from <i>Hordeum</i>		4.8	4.8	4.8							55	44
glucan endo-1,3-beta-D-glucosidase III from <i>Hordeum</i>		4.8	4.8	4.8							70	44
endo-1,4-beta-xylanase from <i>Sporotrichum thermophi</i>	extracellular	5	5	5					6.7			45

laccase from <i>Lentinula edodes</i>	intracellular	3	3	3	3 - 7	5	3	0	6.9		95	46
alpha-amylase from <i>Thermococcus</i> sp.		5	5	5	5 -- 9	7	5	0		450	65	47
beta-glucosidase from <i>Termitomyces clypeatus</i>		5	5	5	2 -- 10	6	5	0	4.5		55	48
3-phytase from <i>Klebsiella terrigena</i>		5	5	5	3.0-9.0	6	5	0	5.5		65	49
alpha-galactosidase from <i>Thermomyces lanuginosus</i>	extracellular	5-5.5	5.25	5.25							30	50
glucan endo-1,3-beta-D-glucosidase from <i>Schizosacc</i>	cell wall	5	5	5								51
dextranase from <i>Sporothrix schenckii</i>	extracellular	4.8- 5.0	4.9	4.9								52
endoglycosylceramidase I from <i>Rhodococcus</i> sp.		5	5	5	4.0 -- 8.0	6	5	0				53
endoglycosylceramidase II from <i>Rhodococcus</i> sp.		5.5	5.5	5.5	5.0 -- 8.5	6.75	5.5	0				53
tannase from <i>Aspergillus niger</i>		5.5-6.5	6	5.5	4.5-6.0	5.25	5.5	0			42.7	54
glucan endo-1,6-beta-glucosidase from <i>Acremonium p</i>		5	5	5	4.5-9.0	6.75	5	0	4.9		45	55
glucan 1,6-alpha-glucosidase from <i>Lipomyces lipofe</i>	extracellular	4.5-5.0	4.75	5	4.5-6.0	5.25	5	0	7		60	56
glucan 1,4-alpha-glucosidase from <i>Aspergillus terr</i>		5	5	5	3.0-8	5.5	5	0				57
L-glutamate oxidase from <i>Streptomyces violascens</i>		5	5	5	3.0-7.0	5	5	0			50	NA
cellulase from <i>Trichoderma viride</i>		4.5-5.0	4.75	5	4.5-7.5	6	5	0			55	58
alpha-L-rhamnosidase from <i>Aspergillus aculeatus</i>	extracellular	4.5-5.0	4.75	4.5	3 -- 5	4	4.5	0			55	59
alpha-galactosidase from <i>Monascus pilosus</i>		4.5 - 5.0	4.75	5	3 -- 8	5	5	0			45	60
alpha-galactosidase I from <i>Oryza sativa</i>		5	5	5	3 -- 8	5	5	0			45	61
alpha-galactosidase II from <i>Oryza sativa</i>		5	5	5	3.5- 8.5	6	5	0			45	61
alpha-galactosidase III from <i>Oryza sativa</i>		5	5	5	4 -- 7	5.5	5	0			60	61
beta-glucosidase from <i>Sclerotinia sclerotiorum</i>		5	5	5	3-8	5	5	0			45	62
poly(beta-D-mannuronate) lyase from <i>Dendryphiella</i>	extracellular	5	5	5	4--10	6.5	5	0	3.65	350	50	63
alpha-galactosidase from <i>Aspergillus nidulans</i>	extracellular	4 --5	4.5	4.5					6.3		55	64
endo-1,4-beta-xylanase from <i>Penicillium citrinum</i>	extracellular	5	5	5	2 -- 10	6	5	0	3.5			65
chitinase from <i>Streptomyces erythraeus</i>	extracellular	5	5	5							55	66
beta-N-acetylhexosaminidase from <i>Bipolaris sorokin</i>	extracellular	4.5	4.5	4.5	4 --10	6.5	4.5	0			65	67
.beta-N-acetylhexosaminidase from <i>Boophilus microp</i>		4.7	4.7	4.7								67
beta-glucuronidase from <i>Mus musculus</i>	lysosome	4.7	4.7	4.7	4 -- 11	7.5	4.7	0			70	68
beta-glucosidase from <i>Aspergillus niger</i>	extracellular	4.6-5.3	4.95	4.95							85	69
beta-galactosidase from <i>Sterigmatomyces elviae</i>	cell wall	4.5-5.0	4.75	4.75	2.5-7	4.75	4.75	0			45	70
aspartate 4-decarboxylase from <i>Pseudomonas</i> sp.		5	5	5	4.0-8.5	6.25	5	0				71
fructan beta-fructosidase from <i>Cryptococcus aureus</i>	extracellular	5	5	5							40	72
endo-1,4-beta-xylanase from <i>Cryptococcus albidus</i>	extracellular	5	5	5							55	73
glucan 1,4-alpha-glucosidase from <i>Paecilomyces var</i>	extracellular	5	5	5							65	74
glucan 1,3-beta-glucosidase from <i>Acremonium persic</i>	extracellular	6.5	6.5	6.5	4.5 -- 10	7.25	6.5	0	5.3		55	75
glucan 1,3-beta-glucosidase from <i>Acremonium persic</i>	extracellular	5	5	5	4.5 -- 10	7.25	5	0	5.1		50	75
glucan 1,3-beta-glucosidase from <i>Acremonium persic</i>	extracellular	5	5	5	4.5 -- 10	7.25	5	0	4.4		60	75
feruloyl esterase from <i>Aspergillus niger</i>		5	5	5	4-9.5	6.75	5	0			50	22
xylan 1,4-beta-xylosidase from <i>Pichia stipitis</i>		5	5	5	3.5-7.2	5.35	5	0			60	76
beta-fructofuranosidase from <i>Candida utilis</i>		5.5	5.5	5.5	3 -- 6	4.5	5.5	0			65	24
alpha,alpha-trehalase from <i>Lobosphaera</i> sp.	intracellular	5.5	5.5	5.5	4 -- 9	6.5	5.5	0			65	77
chitinase I from <i>Bombyx mori</i>		5.5	5.5	5.5	4 -- 10	7	5.5	0			88	78
chitinase II from <i>Bombyx mori</i>		6.5	6.5	6.5	4 -- 10	7	6.5	0			30	78
carboxylesterase from <i>Lactobacillus casei</i>		5.5	5.5	5.5	4.0-8.0	6	5.5	0			55	79
3-phytase from <i>Aspergillus fumigatus</i>		5.5	5.5	5.5								80
deoxyguanosine kinase from <i>Bos taurus</i>		5.5	5.5	5.5	7	7	7		24250		37	81
cathepsin B from <i>Homo sapiens</i>		5.5	5.5	5.5	3.6- 6.5	5.05	5.5	0			50	82
beta-amylase from <i>Xanthophyllomyces dendrorhous</i>	extracellular	5.5	5.5	5.5							50	83
alpha-glucuronidase from <i>Piromonas communis</i>	extracellular	5.5	5.5	5.5							50	NA
fructan beta-fructosidase from <i>Kluyveromyces marxi</i>		5.5	5.5	5.5	4.5-6.5	5.5	5.5	0				84
.chitosanase from <i>Streptomyces</i> sp.		5.5	5.5	5.5	5.5	5.5	5.5	0			60	85

chitosanase from <i>Bacillus</i> sp.	extracellular	5.5	5.5	5.5	7	7	7	1.5		45	86
beta-glucosidase from <i>Bifidobacterium breve</i>	extracellular	5.5	5.5	5.5	5-- 8	7.5	5.5	0	4.3	50	87
Acetylxyran esterase I from <i>Penicillium purpurogen</i>	extracellular	5.3	5.3	5.3						60	88
Acetylxyran esterase II from <i>Penicillium purpuroge</i>	extracellular	6	6	6						60	88
xylan 1,4-beta-xylosidase from <i>Arxula adeninivoran</i>		5	5	5							89
alcohol dehydrogenase (acceptor) from <i>Gluconobacte</i>	membrane	5.5	5.5	5.5	5.8	5.8	5.8	-0.3		60	90
chitin deacetylase from <i>Mortierella</i> sp.	extracellular	5.5	5.5	5.5	4.5 - 8.0	6.25	5.5	0			91
alpha-L-rhamnosidase A from <i>Aspergillus aculeatus</i>		4.5	4.5	4.5	4-5.5	4.75	4.5	0			92
alpha-L-rhamnosidase B from <i>Aspergillus aculeatus</i>		5	5	5	3-5.5	4.75	5	0		27	92
glucuronan lyase from <i>Trichoderma</i> sp.		5.5	5.5	5.5	4 -- 8	6	5.5	0	6.95		93
alpha-glucosidase I from <i>Saccharomyces fibuligera</i>	cell wall	5.5	5.5	5.5	4.0-8.0	6	5.5	0		52.5	94
alpha-glucosidase II from <i>Saccharomyces fibuligera</i>	extracellular	5.5	5.5	5.5	4.0-8.0	6	5.5	0		60	94
alpha-glucuronidase from <i>Thermoanaerobacterium</i> sp.		5.4	5.4	5.4	6.2-7.9	7.05	6.2	0	4.65		95
pullulanase from <i>Clostridium thermohydrosulfuricum</i>	membrane	5.5	5.5	5.5	3.0-5.0	4	5	0.5		55	96
alpha-N-arabinofuranosidase from <i>Aspergillus nidul</i>	extracellular	5.5	5.5	5.5					4.3		97
adenosine kinase from <i>Homo sapiens</i>		5.5	5.5	5.5	7.4	7.4	7.4	-1.9		45	98
aspartate 4-decarboxylase from <i>Pseudomonas</i> sp.	intracellular	5.5	5.5	5.5						25	99
tannase I from <i>Verticillium</i> sp.		5.5	5.5	5.5	3.5 - 8.0	5.75	5.5	0		20	100
tannase II from <i>Verticillium</i> sp.		5.5	5.5	5.5	3.5 - 8.0	5.75	5.5	0			100
beta-amylase from <i>Clostridium thermosulfurogenes</i>	extracellular	5.5	5.5	5.5	3.5-7.0	5.75	5.5	0	5.1		101
glucan 1,4-beta-glucosidase from <i>Chaetomium olivac</i>		5.2	5.2	5.2						60	102
2,6-beta-fructan 6-levanbiohydrolase from <i>Streptom</i>	extracellular	5.5	5.5	5.5	3.5-8.0	5.75	5.5	0	4.7		103
alpha-L-fucosidase from <i>Bacillus circulans</i>	extracellular	5.5-6.5	6	6.5	4.5-9.0	6.75	6.5	0		50	104
4-phytase from <i>Aspergillus japonicus</i>	extracellular	5.5	5.5	5.5	2.0-8.0	5	5.5	0		70	105
cyclomaltodextrin glucanotransferase from <i>Paenibac</i>		5.5 & 9.0	7.25	7.75	4.5 - 11.0	7.75	7.75	0		60	106
fructan beta-fructosidase from <i>Aspergillus fumigat</i>		5.5	5.5	5.5	4.0 - 9.5	6.75	5.5	0	8.8		107
dextrin dextranase from <i>Gluconobacter oxydans</i>	extracellular	5.2	5.2	5.2	4.1-5.4	4.75	5.2	0			108
aryl-alcohol oxidase from <i>Pleurotus eryngii</i>		6	6	6	6-9.0	7.5	6	0		70.5	109
aryl-alcohol oxidase from <i>Pleurotus pulmonarius</i>		6	6	6	6-9.0	7.5	6	0	3.95		110
cyclomaltodextrin glucanotransferase from <i>Bacillus</i>	extracellular	5.5	5.5	5.5					6.7		111
dextranucrase I from <i>Leuconostoc mesenteroides</i>		6	6	6						35	112
dextranucrase N from <i>Leuconostoc mesenteroides</i>		5.5	5.5	5.5							112
gluconate 5-dehydrogenase from <i>Gluconobacter subox</i>	membrane	6	6	6	5	5	5	1			113
sucrose synthase from <i>Zea mays</i>		6	6	6	5.5-8.0	6.75	6	0			114
adenylate kinase from <i>Bos taurus</i>		5.8 forward	5.8	5.8	5-11	8	5.8	0	9.3		115
triacylglycerol lipase from <i>Pseudomonas aeruginosa</i>		6	6	6	5-8	6.5	6	0			116
pullulanase from <i>Geobacillus stearothermophilus</i>	extracellular	6	6	6	6.0-8.5	7.25	6	0		75	117
alpha-glucosidase from <i>Bacillus thermoglucosidasius</i>	extracellular	5.0-6.0	5.5	6	4.0-11 @ 31 C & 6.0- 8.5 @ 55.5 C	7.5	6	0		55	118
chitinase from <i>Bacillus licheniformis</i>		6 & 8	7	6.5	4.0-9.0	6.5	6.5	0			119
acylaminocyl-peptidase from <i>Homo sapiens</i>	cytosol	8.3	8.3	8.3	6.0-8.0	7	8	0.3		45	120
phospholipase D from <i>Streptomyces</i> sp.		6	6	6	7-9.	8	7	0		60	121
xylan 1,4-beta-xylosidase from <i>Geobacillus stearot</i>		7	7	7	5-11	8	7	0		70	122
xylan 1,4-beta-xylosidase BETA from <i>Geobacillus stearot</i>		6	6	6	6.0-8	7	6	0		90	122
carboxylesterase from <i>Sulfolobus shibatae</i>		6	6	6							123
alpha-N-arabinofuranosidase from <i>Pichia capsulata</i>	intracellular	6	6	6	7	7	7	-1		50	124
beta-glucosidase I from <i>Penicillium aurantiogriseu</i>	extracellular	6	6	6	5.0-7.5	6.25	6	0	3.6		125
beta-glucosidase II from <i>Penicillium aurantiogriseu</i>	extracellular	6	6	6	5.5-7.5	6.5	6	0	3.4		125
cathepsin H from <i>Homo sapiens</i>		6.8	6.8	6.8	up to 7				6		126
salutaridine reductase (NADPH) from <i>Papaver somnif</i>		6	6	6	5.5-6.5	6	6	0		50	
beta-N-acetylhexosaminidase from <i>Vibrio furnissii</i>	periplasm	5.8	5.8	5.8						40	127

aldehyde dehydrogenase (pyrroloquinoline-quinone)	membrane	5	5	5	7	7	7	-2		42	128
.alpha-mannosidase from <i>Candida albicans</i>		6	6	6						50	129
.exo-1,4-beta-D-glucosaminidase from <i>Aspergillus f</i>	extracellular	3-6.0	4.5	6	2-10	6	6	0			130
dipeptidyl-peptidase II from <i>Sus scrofa</i>		6	6	6	3.5-10	6.75	6	0		40	131
alpha-L-rhamnosidase from <i>Pichia angusta</i>		6	6	6	6 (5--7 peak at 6)	6	6	0	4.9		132
alpha-galactosidase from <i>Spodoptera frugiperda</i>		5.8	5.8	5.8	5	5	5	-0.8	7.2		133
mannosyl-glycoprotein endo-beta-N-acetylglucosamin		6.0-7.5	6.75	7	7	7	7	0			
mannosyl-glycoprotein endo-beta-N-acetylglucosamin		4.5-6.0	5.25	5.5	5.5	5.5	5.5	0		55	
inulin fructotransferase (DFA-III-forming) from <i>Ba</i>		6	6	6						60	
beta-galactosidase from <i>Bacillus circulans</i>		5-6	5.5	6	5-9	7	6	0			134
endoglycosylceramidase from <i>Rhodococcus sp.</i>		6	6	6	5 -- 9	7	6	0		50	135
endo-1,4-beta-xylanase from <i>Aspergillus ochraceus</i>		6	6	6	5 --10	7.5	6	0			36
alpha-L-fucosidase from <i>Bos taurus</i>		5.6	5.6	5.6	4.5-6	5.25	5.6	0		35	136
extracellular agarase from <i>Vibrio sp.</i>		6	6	6	4.0-8.0	6	6	0		45	137
alpha-N-arabinofuranosidase from <i>Butyrivibrio fibr</i>		6.0-6.5	6.25	6	4.0-8.0	6	6	0	6	55	138
alpha-amylase from <i>Lactobacillus manihotivorans</i>		5.5	5.5	5.5	5-6.	5.5	5.5	0		50	139
beta-glucosidase from <i>Stachybotrys sp.</i>		6	6	6	4 --10	7	6	0		64	140
mannan 1,4-mannobiosidase from <i>Aeromonas hydrophil</i>		6	6	6	5.0-8.5	6.75	6	0	5.9	85	141
pullulanase from <i>Clostridium thermohydrosulfuricum</i>		5.6	5.6	5.6							142
adenosine deaminase from <i>Streptomyces sp.</i>	cytosol	5.8	5.8	5.8						97	
alpha-amylase from <i>Streptomyces megasporus</i>		6	6	6	5.5-8.5	7	6	0	5.4		143
6G-fructosyltransferase from <i>Allium cepa</i>		5.7	5.7	5.7	5.3-6.3	5.8	5.7	0			144
memapsin 1 from <i>Homo sapiens</i>		6	6	6	4-12	8	6	0		90	145
pullulanase from <i>Thermoanaerobacter ethanolicus</i>		6	6	6	5.0 & 5.5	5.25	6	0.5		65	146
cellulase CH43 from <i>Bacillus sp.</i>		5- 6.5	5.75	6.5	6-10	8	6.5	0	5.4	70	147
cellulase HR68 from <i>Bacillus sp.</i>		5-6.5	5.75	6.5	6-8	7	6.5	0	5.4	45	147
dextranucrase I from <i>Leuconostoc mesenteroides</i>		6.3-6.5	6.4	6.4						35	148
dextranucrase II from <i>Leuconostoc mesenteroides</i>		5.5-5.9	5.7	5.7							148
morphine 6-dehydrogenase from <i>Cavia porcellus</i>			6.8 w/ NADPH and 6.2 w/NADH	6.2	6.2	6	6	0.8		50	149
beta-galactosidase L103 from <i>Lactobacillus reuter</i>		8	8	8	6	6	6	2	3.8	50	150
beta-galactosidase L461 from <i>Lactobacillus reuter</i>		8	8	8	6-6.5	6.25	6.5	1.5	4.6		150
endo-1,4-beta-xylanase from <i>Geobacillus stearothermophilus</i>		6.5	6.5	6.5	7	7	7	-0.5			151
cathepsin B from <i>Homo sapiens</i>		6.2-6.4	6.3	6.2	5	5	5	1.2		50	152
adenosine deaminase from <i>Nocardiooides sp.</i>		6	6	6	6.5-7.5	7	6	-0.5	7.6	75	153
beta-N-acetylhexosaminidase from <i>Geobacillus stearothermophilus</i>		6.5	6.5	6.5	6.5	6.5	6.5	0			154
mannosyl-glycoprotein endo-beta-N-acetylglucosamin		6.0-6.5	6.25	6.5	7--8	7.5	6.5	0			155
cathepsin L1 from <i>Fasciola hepatica</i>		6.2	6.2	6.2	4.5	4.5	4.5	1.7		55	156
bacillolysin from <i>Bacillus nematocida</i>		6.5	6.5	6.5	5--8	6.5	6.5	0		23.6	157
endo-1,4-beta-xylanase from <i>Thermomyces lanuginosus</i>		6.5	6.5	6.5	5 --12	8.5	6.5	0	3.8		158
myosin-light-chain kinase from <i>Oryctolagus cuniculus</i>		6.5	6.5	6.5	6.3-8	7.15	6.5	0			159
deoxyribonuclease I from <i>Homo sapiens</i>		6.5	6.5	6.5	5--9	7	6.5	0			160
glycerol-3-phosphate dehydrogenase (NAD+) from <i>Try</i>		6.5	6.5	6.5	5 --9	7	6.5	0			161
cathepsin H I from <i>Rattus norvegicus</i>		6.5	6.5	6.5	5 --9	7	6.5	0			162
cathepsin H II from <i>Rattus norvegicus</i>		7	7	7	5 --9	7	7	0			162
cathepsin H III from <i>Rattus norvegicus</i>		6.5	6.5	6.5	5 --9	7	6.5	0		45	162
4-alpha-D-{(1->4)-alpha-D-glucano}trehalose trehal		6.5	6.5	6.5	5--10	7	6.5	0	4.1		163
AMP deaminase from <i>Oryctolagus cuniculus</i>		6.4	6.4	6.4	6.8	6.8	6.8	-0.4			164
inositol 2-dehydrogenase from <i>Acetomonas oxydans</i>		6.2	6.2	6.2	6.8	6.8	6.8	-0.6			165
NADH dehydrogenase (ubiquinone) from <i>Trypanosoma b</i>		6.0-6.5	6.25	6.5	4.5-9.5	7	6.5	0			166

beta-galactoside alpha-2,3-sialyltransferase from		6.0-6.5	6.25	6.25	6.0-6.5	6.25	6.25	0			65	167
endoglycosylceramidase from Corynebacterium sp.		5.5-6.5	6	5.75	3.5-8.0	5.75	5.75	0			40	168
D-Arabinono-1,4-lactone oxidase from Candida albic		8	8	8	4.5-7.5	6	7.5	0.5	5		50	169
chitinase from Orpinomyces sp.	cytosol	6.5	6.5	6.5	4.5-7.0	5.75	6.5	0			40	170
chitinase from Anaeromyces sp.	cytosol	6.5	6.5	6.5	4.5-7.0	5.75	6.5	0			30	170
ribonuclease [poly-(U)-specific] from Biziozia sp.		6.5	6.5	6.5	7	7	7	-0.5				171
alpha-1,6-mannosyl-glycoprotein 6-beta-N-acetylglu		6.5	6.5	6.5	7	7	7	-0.5			75	81
endo-1,4-beta-xylanase from Clostridium thermolact		6.0-6.5	6.25	6.5	3-11	7	6.5	0	4.9		37	172
glycosylceramidase from Sus scrofa		6.5-7.0	6.75	7	8 -- 11	9.5	8	0				173
licheninase from Orpinomyces sp.		5.8-6.2	6	6.2	3.4-9.8	6.6	6.2	0			65	174
cyclomaltodextrin glucanotransferase from Paenibac		6.5	6.5	6.5	6.0-11.5	8.75	6.5	0			43	175
alpha-amylase from Bacteroides amylophilus		6.3	6.3	6.3	5.8-7.5	6.65	6.3	0	4.6		50	176
beta-glucosidase from Volvariella volvacea		6.4	6.4	6.4	5.6-8.0	6.8	6.4	0			60	177
alpha-N-arabinofuranosidase from Bacillus pumilus		6.4	6.4	6.4	5.2-7.6	6.4	6.4	0			90	178
endo-1,4-beta-xylanase from Sulfolobus solfataricu		7	7	7							60	179
glucan endo-1,3-beta-D-glucosidase from Aspergillu		7	7	7	8 -- 10	9	7	0				180
phosphatidylinositol diacylglycerol-lyase from Hom		7	7	7	5 -- 11	8	7	0			37	181
carboxylesterase from Lactobacillus casei		7	7	7	6-8	7	7	0			40	182
glutathione-disulfide reductase from Thiobacillus	mitochondrian	7	7	7	6-8	7	7	0			36	NA
deacetoxyccephalosporin-C synthase from Streptomyce		7.4	7.4	7.4	6.5-9.0	7.75	7.4	0			25	183
poly(beta-D-mannuronate) lyase from Vibrio sp.		7	7	7	6.0-7.5	6.75	7	0				71
1,4-alpha-glucan branching enzyme from Phaseolus v		7	7	7	7.0-9.0	8	7	0			60	184
beta-amylase from Bacillus megaterium	extracellular	6.9	6.9	6.9								185
glycoprotein 2-beta-D-xylosyltransferase from Glyc	microsome	7	7	7	7	7	7	0				186
electron-transferring-flavoprotein dehydrogenase f		7	7	7	7.8	7.8	7.8	-0.8			20	187
glutathione transferase from Bos taurus		7	7	7	6.5	6.5	6.5	0.5			36	188
alliin lyase from Allium sativum		7	7	7							50	189
dipeptidyl-peptidase IV from Lactococcus lactis		7	7	7								190
carboxylesterase from Geobacillus stearothermophil		7	7	7	6.0-8.9	7.45	7	0	5.8		37	191
licheninase from Bacillus sp.		6.8 for neutral invertase	6.8	6.8	7.0-8.0	7.5	7	0				192
alpha-amylase from Fusicoccum sp.		7	7	7	7	7	7	0			60	193
aculeacin-A deacetylase from Actinoplanes utahensis		7	7	7				0				194
carboxypeptidase M from Homo sapiens		7	7	7	4.5-5.0	4.75	5	2			50	195
1,2-alpha-L-fucosidase from Bacillus cereus	extracellular	7	7	7	5.0-9.0	7	7	0				196
poly(ADP-ribose) glycohydrolase from Bos taurus	nucleus	7.0-7.5	7.25	7	5.0-9.0	7	7	0			40	197
cellulase from Ruminococcus albus	cell surface	7	7	7								198
monophenol monooxygenase from Streptomyces sp.		6.8	6.8	6.8					9.9		37	199
xylan endo-1,3-beta-xylosidase from Vibrio sp.		7	7	7	5.0-8.0	6.5	7	0	3.6			200
glucan 1,4-beta-glucosidase from Thermomonospora s	extracellular	7	7	7	5.0-8.0	6.5	7	0			36	201
chitosanase from Acinetobacter sp.	extracellular	7	7	7	5.0-8.0	6.5	7	0				202
glutathione transferase from Taenia solium	microsome	6.6	6.6	6.6	6.0-7.5	6.75	6.6	0			37	203
poly(alpha-L-guluronate) lyase from Klebsiella aer		7	7	7							50	204
chitin deacetylase from Aspergillus nidulans		7	7	7	4.0-7.5	5.75	7	0			55	205
poly(alpha-L-guluronate) lyase from Corynebacteriu		7	7	7	4.0-10	7	7	0	7.3			206
Xaa-Pro aminopeptidase from Rattus norvegicus		6.8-7.5	7.15	7.5	7.0-10.5	8.75	7.5	0			70	207
chitinase from Thermococcus chitonophagus	membrane	7	7	7	3.0-9.0	6	7	0	5.9		65	208
cholesterol oxidase from Chromobacterium sp. DS-1		7	7	7	3.0-11.0	6.5	7	0				209
biliverdin reductase from Rattus norvegicus	cytoplasm	8.7 NADPH	8.7	8.7	7.4	7.4	7.4	1.4				210
2-aminomuconate deaminase from Pseudomonas pseudoa	cytoplasm	6.6	6.6	6.6	5.7-8.8	7.25	6.6	0			60	211

galacturan 1,4-alpha-galacturonidase from <i>Bacillus</i>		7	7	7	7.0-12	9.5	7	0			212
mannose-6-phosphate 6-reductase from <i>Apium graveol</i>		7.5 with m6p/nadph	7.5	7.5	6.0-9.0	7.5	7.5	0		50	213
chitinase from <i>Bacillus sp.</i>		8.5	8.5	8.5	5.0-10.0	7.5	8.5	0			214
arylesterase from <i>Rattus norvegicus</i>		8.8	8.8	8.8	5.0-10.0	7.5	8.8	0		55	215
glutamyl endopeptidase from <i>Bacillus intermedius</i>		7.5 for casein	7.5	7.5	6.5-11	8.75	7.5	0		45	216
phospholipase D from <i>Streptomyces sp.</i>		7.5	7.5	7.5	6.0-8.0	7	7.5	0		35	217
phospholipase D from <i>Streptomyces sp.</i>					6.0-8.0	7	7				217
D-amino-acid oxidase from <i>Trigonopsis variabilis</i>		7.5	7.5	7.5	9.5	9.5	9.5	-2			218
thymidine kinase from <i>Homo sapiens</i>		7.4-7.8	7.6	7.8	7.0-9.0	8	7.8	0			219
D(-)-tartrate dehydratase from <i>Rhodopseudomonas sp</i>		6.2-7.2	6.7	7.2	6.0-8.7	7.35	7.2	0		35	220
tocopherol O-methyltransferase from <i>Euglena gracil</i>		7.5	7.5	7.5							221
L-xylulose reductase from <i>Cavia porcellus</i>		7.5	7.5	7.5	4.0-9.0	6.5	7.5	0		60	222
bacillolysin from <i>Bacillus megaterium</i>		7.4	7.4	7.4							223
aspartyl aminopeptidase from <i>Plasmodium falciparum</i>		7.5	7.5	7.5					6		224
.beta-N-acetylhexosaminidase from <i>Cellulomonas fim</i>		7.3-8.7	8	8					6		225
glycine C-acetyltransferase from <i>Bos taurus</i>		7.5	7.5	7.5	6.5-8.0	7.25	7.5	0	5.2	40	226
beta-glucosidase from <i>Pichia pastoris</i>		7.3	7.3	7.3	5.5-9.5	7.5	7.3	0		22	227
carboxylesterase from <i>Pseudomonas sp.</i>	intracellular	7.5	7.5	7.5					5.9	30	228
triacylglycerol lipase from <i>Arxula adeninivorans</i>		7.5	7.5	7.5	7.0-7.5	7.25	7.5	0		35	229
tetrachloroethene reductive dehalogenase from <i>Clos</i>	cytoplasmic membrane	7.5	7.5	7.5	7.5-8.0	7.75	7.5	0			230
2-nitrophenol 2-monooxygenase from <i>Pseudomonas put</i>		7.5-8.0	7.75	7.75	7.5-8.0	7.75	7.75	0		48	231
6-aminohexanoate-dimer hydrolase from <i>Pseudomonas</i>		7.5	7.5	7.5	6.8-8.5	7.65	7.5	0			232
glycogen(starch) synthase from <i>Homo sapiens</i>		6.8	6.8	6.8	6.8-7.6	7.2	6.8	0			233
urate oxidase from <i>Arthrobacter globiformis</i>		7.0-7.5	7.25	7.5	8.5-11.0	9.75	8.5	0			234
oligosaccharide reducing-end xylanase from <i>Bacillu</i>		7	7	7	7	7	7	0		37	235
carboxylesterase from <i>Bacillus subtilis</i>		8	8	8	6.0-9.0	7.5	8	0		65	236
aminoacylase from <i>Alcaligenes sp.</i>		8	8	8							237
glucose 1-dehydrogenase from <i>Bacillus subtilis</i>		8	8	8	6.5	6.5	6.5	1.5		37	238
beta-diketone hydrolase from <i>Sphingomonas sp.</i>		8	8	8	6.5-8.5	7.5	8	0			239
triacylglycerol lipase from <i>Aureobasidium pullulan</i>		8	8	8	4.0-9.0	6.5	8	0		55	240
chitinase from <i>Bacillus licheniformis</i>		6	6	6	4	4	4	2			119
phosphatidylinositol diacylglycerol-lyase from <i>Hom</i>		7	7	7	5.0-11.0	8	7	0			181
carboxylesterase from <i>Sulfolobus shibatae</i>		7.0-8.0	7.5	7	6.0-8.0	7	7	0		94	241
creatinase from <i>Pseudomonas putida</i>		8	8	8	6.0-8.0	7	8	0			242
prostaglandin-endoperoxide synthase from <i>Bos tauru</i>		8	8	8	6.0-8.0	7	8	0		87	243
.beta-mannosidase from <i>Thermotoga neapolitana</i>		7.7	7.7	7.7						100	244
beta-mannanase from <i>Thermotoga neapolitana</i>		7.3	7.3	7.3						90	244
alpha-galacosidase from <i>Thermotoga neapolitana</i>		6.9	6.9	6.9						70	244
Arylalkyl acylamidase from <i>Pseudomonas putida</i>		8	8	8	>7					50	245
phospholipase C1from <i>Streptomyces hachijoensis</i>	extracellular	8	8	8	7	7	7	1	6	60	246
alkan-1-ol dehydrogenase (acceptor) from <i>Pseudomon</i>		8	8	8	7.5-9.0	8.25	8	0			247
2,6-dihydroxypyridine 3-monooxygenase from <i>Arthrob</i>		8	8	8	7	7	7	1			248
superoxide dismutase from <i>Triticum aestivum</i>		8	8	8	7.0-9.0	8	8	0		37	249
1-deoxy-D-xylulose-5-phosphate reductoisomerase fr		8	8	8	7.5	7.5	7.5	0.5			250
anthocyanin 5-O-glucoside 6'''-O-malonyltransferas		8	8	8	7.5	7.5	7.5	0.5		40	251
triacylglycerol lipase from <i>Acinetobacter sp.</i>		8	8	8	6.0-10.0	8	8	0		55	252
type II site-specific deoxyribonuclease from <i>Esche</i>		8	8	8	6.0-10.0	8	8	0		55	253
Acetylxylan esterase from <i>Bacillus pumilus</i>	extracellular	8	8	8	8.0-9.5	8.75	8	0	4.8		254
.L-glutamate oxidase from <i>Streptomyces endus</i>	extracellular	6.5-8.0	7.25	6.5	5.5-7.5	6.5	6.5	0.5		55	255
NAD+ kinase from <i>Homo sapiens</i>		7.5	7.5	7.5							256

2',3'-cyclic-nucleotide 2'-phosphodiesterase from											257
dihydroorotate dehydrogenase from Bos taurus		8	8	8	6.5-10.5	8.5	8	0		45	258
3-hexulose-6-phosphate synthase from Methylomonas		8	8	8							259
procollagen N-endopeptidase from Gallus gallus		7.9-8.3	8.1	7.9	5.5-10.0	7.75	7.9	0		45	260
nitrilase from Aspergillus niger		8	8	8	7.2-9.0	8.1	8	0		25	261
alcohol O-acetyltransferase from Saccharomyces cerevisiae		8	8	8	7.5-8.5	8	8	0		37	262
poly(beta-D-mannuronate) lyase from Bacillus sp.		7.5	7.5	7.5							263
penicillin amidase from Bacillus megaterium		8.0-9.0	8.5	8.25	6.5-10.0	8.25	8.25	0			264
gingipain K from Porphyromonas gingivalis		8.0-8.5	8.25	8.25	8.0-8.5	8.25	8.25	0		40	265
beta-agarase from Agarivorans albus		8	8	8	6.0-11.0	8	8	0		40	266
serine-glyoxylate transaminase from Hyphomicrobium		8	8	8	6.0-11.0	8.5	8	0			267
nicotinate phosphoribosyltransferase from Homo sapiens		6.5-8.0	7.25	7.5	5.0-10.0	7.5	7.5	0		37	268
triacylglycerol lipase from Rhizopus oryzae		8	8	8	5.0-8.0	6.5	8	0			269
nucleoside-triphosphate-aldehyde-1-phosphate nucleotidase		7.5-8.0	7.75	7.5	6.0-6.5	6.25	6.5	1			270
peptidase K (PRK) from Tritirachium album		8	8	8	4.0-12	8	8	0			271
peptidase K (SPRK) from Tritirachium album		10.5	10.5	10.5	5.5-9.5	7.5	9.5	1			271
ornithine carbamoyltransferase from Rattus norvegicus		7.6-8.1	7.95	7.95	6.8-9.0	7.9	7.95	0		39	272
chlorophyllase from Secale cereale					6.0-9.0	7.5	7.5		4.5		273
hepacivirin from hepatitis C virus		8.0-8.5	8.25	8	7.5	7.5	7.5	0.5			274
mannose-6-phosphate 6-reductase from Apium graveolens		8.5	8.5	8.5	6.0-9.0	7.5	8.5	0			213
D-amino-acid oxidase from Rhodotorula gracilis		8.5	8.5	8.5	6.0-9.0	7.5	8.5	0		30	275
alcohol oxidase from Aspergillus terreus		8.5	8.5	8.5	6.0-11.0	8.5	8.5	0		65	276
cyclomaltodextrin glucanotransferase from Bacillus		5.5-8.5	7	8.5	7.0-11.0	9	8.5	0			277
branched-chain-amino-acid transaminase from Sus scrofa		8.25	8.25	8.25	6.0-7.0	6.5	6.25	1.25			278
triacylglycerol lipase from Staphylococcus simulans		8.5	8.5	8.5	4.0-9.0	6.5	8.5	0			279
poly(alpha-L-guluronate) lyase from Alteromonas sp.		7.5-8.0	7.75	8	5.0-11.0	8	8	0		50	280
D-amino-acid oxidase from Trigonopsis variabilis		8.5	8.5	8.5	8.5	8.5	8.5	0			281
uracil/thymine dehydrogenase from Mycobacterium sp.		8.5	8.5	8.5	9.0 (alkaline)	9	9	0.5		37	282
triacylglycerol lipase from Acinetobacter sp.		8.5	8.5	8.5	3.0-9.0	6	8.5	0			283
phosphoribosylglycinamide formyltransferase from E. coli		8	8	8	6.0-10.0	8	8	0		50	284
4-aminobutyrate transaminase from Streptomyces griseus		7.5-8.5	8	8	6.0-10.0	8	8	0		53	285
acrosin from Sus scrofa		8.5	8.5	8.5	3	3	3	5.5			286
Thermomycolin from Malbranchaea pulchella		8.5	8.5	8.5	6.5-9.5	8	8.5	0	6	60	287
gamma-glutamyltransferase from Bacillus subtilis		8.5	8.5	8.5	6-8.0	7	8	0.5			288
acrosin from Homo sapiens		8.2	8.2	8.2	3.2	3.2	3.2	3		30	289
pectate lyase from <i>Mrakia frigida</i>		8.5-9.0	8.75	8.5	7.0-10.0	8.5	8.75	0			290
DNA topoisomerase from <i>Saccharomyces cerevisiae</i>		7.5-8.5	8	7.5	5	5	5	2.5			291
glutaryl-CoA dehydrogenase from <i>Paracoccus denitrificans</i>		8.0-8.5	8.25	8	5	5	5	3	4	35	292
urate oxidase from <i>Streptomyces cyanogenus</i>		8	8	8							293
carbon-monoxide dehydrogenase (acceptor) from Rhodopseudomonas palustris		8.6	8.6	8.6	6.5-9.5	8	8.6	0			294
D-amino-acid oxidase from <i>Cyprinus carpio</i>		8.5	8.5	8.5	6.5-11	8.25	8.5	0		50	295
endo-1,4-beta-xylanase from <i>Penicillium citrinum</i>		8.5	8.5	8.5	4.0-10.0	7	8.5	0		55	296
triacylglycerol lipase from <i>Bacillus coagulans</i>	extracellular	8.5	8.5	8.5	8.0-10.5	9.25	8.5	0			297
sulfite oxidase from <i>Bos taurus</i>	mitochondrion	8.5	8.5	8.5	7.0-9.5	8.25	8.5	0			298
1,4-lactonase from <i>Homo sapiens</i>		8.5	8.5	8.5	4.5-9.0	6.75	8.5	0			299
beta-ureidopropionate from <i>Pseudomonas putida</i>	cytosol	7.5-8.2	7.85	7.5	6.1-8.6	7.35	7.85	0			300
protein-glutamine gamma-glutamyltransferase from <i>R. solani</i>		9	9	9	6.0-9.0	7.5	9	0			301
lysophospholipase from <i>Mus musculus</i>		8.0-9.0	8.5	8	6.0-8.5	7.25	8.5	0		40	302
triacylglycerol lipase from <i>Burkholderia cepacia</i>		9	9	9	9.0-10.0	9.5	9	0		60	303
sulfur reductase from thermophilic iron-oxidizing bacteria		9	9	9						35	304
phenylacetaldehyde dehydrogenase from <i>Brevibacteri</i>		9	9	9	6.0-8.0	7	8	1			305

D-amino-acid oxidase from <i>Sus scrofa</i>		9.0-10.0	9.5	9	5.5-9.0	7.25	9	0			50	306
leucyl aminopeptidase from <i>Vibrio</i> sp.		7.8	7.8	7.8							37	307
ferredoxin-NADP+ reductase from <i>Escherichia coli</i>		8.5-9.0	8.75	8.5	6.5-7.5	7	7.5	1				308
4-aminobutyrate transaminase from <i>Pseudomonas fluo</i>		8.5-8.9	8.7	8.5	6.5-7.5	7	7.5	1				309
poly(3-hydroxybutyrate) depolymerase from <i>Comamona</i>		9	9	9	6.0-10.0	8	9	0				310
inorganic diphosphatase from <i>Sesamum indicum</i>		8.6	8.6	8.6	6.0-10.0	8	8.6	0			55	311
glucan 1,4-alpha-maltotriohydrolase from <i>Natronoco</i>		8.7	8.7	8.7	6.0-8.6	7.3	8.6	0.1			45	312
chitin oligosaccharide deacetylase from <i>Vibrio par</i>		8.5-9.0	8.75	8.5	5.0-10.0	7.5	8.75	0				313
Propionyl-CoA carboxylase from <i>Homo sapiens</i>		7.2-8.8	8	8	6.2-8.4	7.3	8	0			60	314
pullulanase from <i>Bacillus</i> sp.		9	9	9	4.0-11.0	7	9	0				315
t-Plasminogen activator from <i>Homo sapiens</i>		7.5	7.5	7.5	5.0-10.0	7.5	7.5	0			52.5	316
1,4-lactonase from <i>Rattus norvegicus</i>		8.8	8.8	8.8	5.0-10.0	7.5	8.8	0				215
nicotinamide phosphoribosyltransferase from <i>Rattus</i>		8.5-9.0	8.75	8.5	7.0-10.0	8.5	8.75	0				317
diamine N-acetyltransferase from <i>Candida boidinii</i>		8.5-9.0	8.75	8.5	7.0-7.5	7.25	7.5	1				318
diamine N-acetyltransferase from <i>Candida boidinii</i>		9.0-9.5	9.25	9.25							55	318
carboxylesterase from <i>Pseudomonas aeruginosa PAO1</i>		9	9	9	5	5	5	5				319
peptidyl-Lys metalloendopeptidase from <i>Myxobacter</i>		8.5-9.0	8.75	8.5	3.0-9.0	6	8.75	0				320
triacylglycerol lipase from <i>Psychrobacter</i> sp.	extracellular	9	9	9	7.0-10.0	8.5	9	0			50	321
glutaminase from <i>Aspergillus oryzae</i>		8.5	8.5	8.5	7.0-9.0	8	8.5	0				322
glycerol-3-phosphate cytidylyltransferase from Bac		7.5	7.5	7.5	9	9	9	1.5			65	81
pectate lyase from <i>Bacillus subtilis</i>		8.7-10.0	9.15	9.7	9.4-10.0	9.7	9.15	0				323
Thermitase from <i>Thermoactinomyces vulgaris</i>	extracellular	7.5-9.5	8.5	7.5	6.0-7.5	6.75	7.5	0				324
Xaa-His dipeptidase from <i>Homo sapiens</i>		9.5	9.5	9.5	7.2-8.2	7.7	8.2	1.3				325
galactose 1-dehydrogenase from <i>Pseudomonas fluores</i>		9.1-9.5	9.3	9.1	6.5-7.6	7.05	7.6	1.5				326
alpha-amylase from <i>Alkalimonas amylolytica</i>		9.5	9.5	9.5	8.5-11.0	9.75	9.5	0			60	327
alcohol dehydrogenase from <i>Zea mays</i>		6	6	6	6.0-9.0	7.5	6	0				NA
serralysin from <i>Escherichia freundii</i>		10	10	10	7	7	7	3				328
glycerol kinase from <i>Escherichia coli</i>		9.8	9.8	9.8	7	7	7	2.8				282
cyclomaltodextrin glucanotransferase from <i>Bacillus</i>		8.0-10.0	9	9.5	7.0-12.0	9.5	9	0				329
alcohol oxidase from <i>Gloeophyllum trabeum</i>		6.5	6.5	6.5	7.0-11.0	9	7	0.5			70	330
catalase from <i>Bacillus</i> sp.		10	10	10	6.0-10.8	8.4	10	0				331
duodenase from <i>Bos taurus</i>		8.0-10.0	9	8	3.0-10.0	6.5	9	0				332
acyl-CoA hydrolase from <i>Alcaligenes faecalis</i>		10.5	10.5	10.5	5.5	5.5	5.5	5				333
triacylglycerol lipase from <i>Pseudomonas aeruginosa</i>		11	11	11	4.5-11.0	7.25	11	0				334

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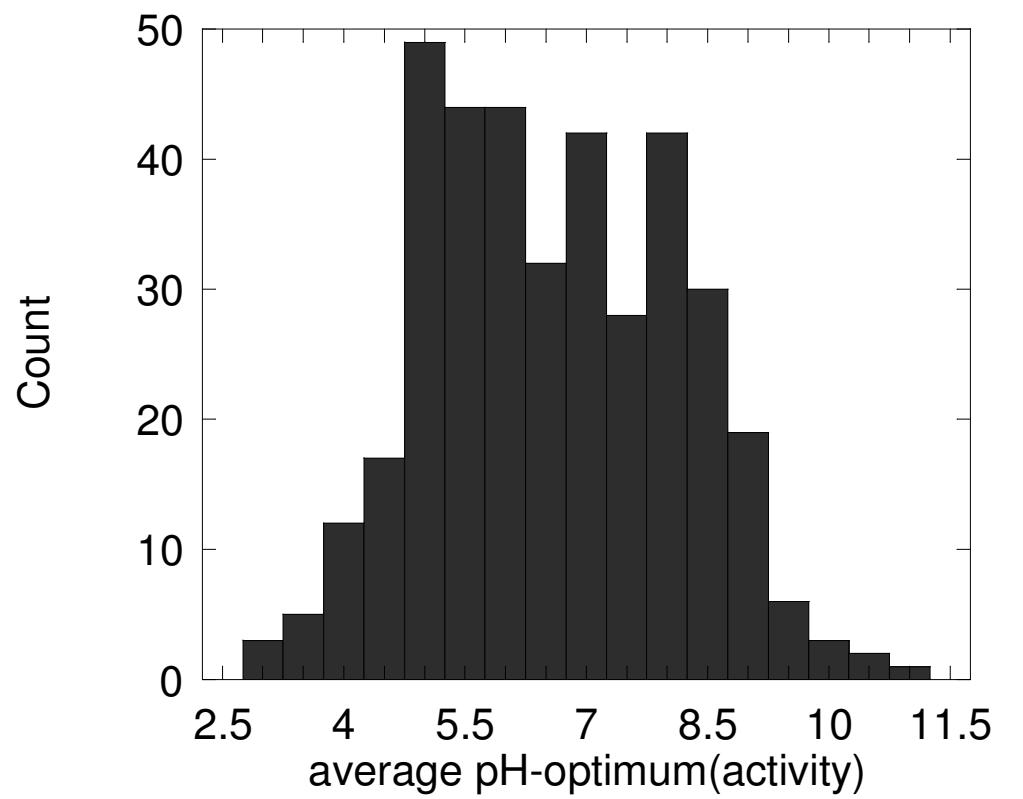


Fig. 1S. The distribution of the average pH-optimum of activity

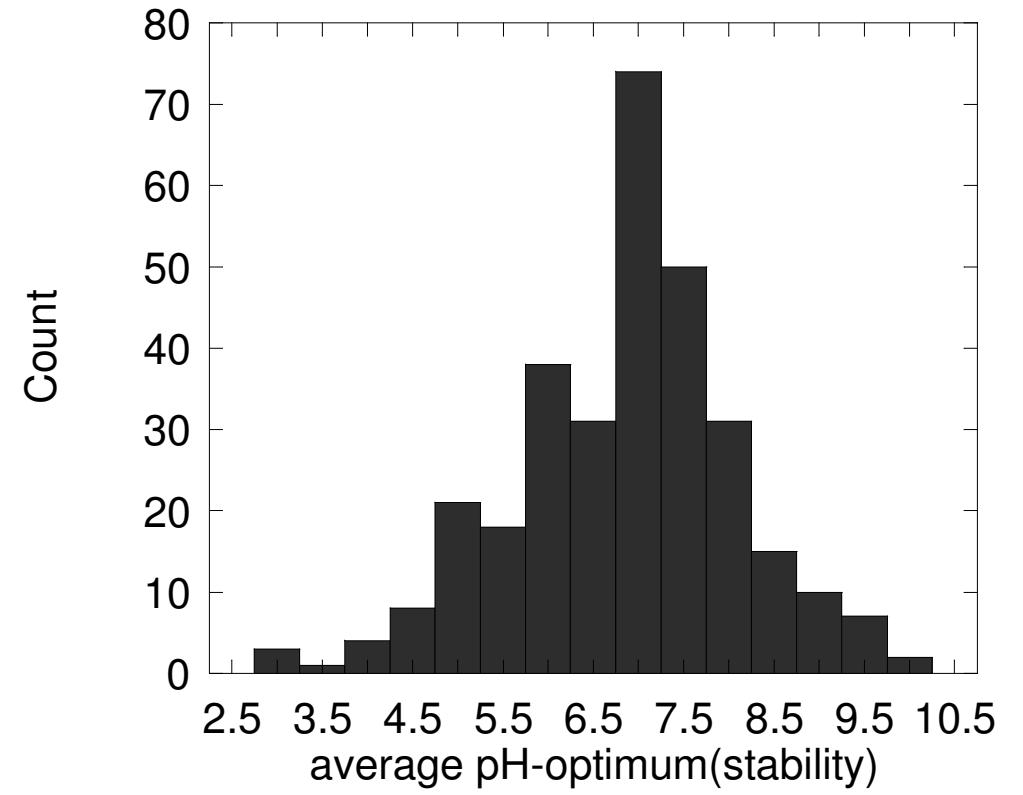


Fig. 2S. The distribution of the average pH-optimum of stability

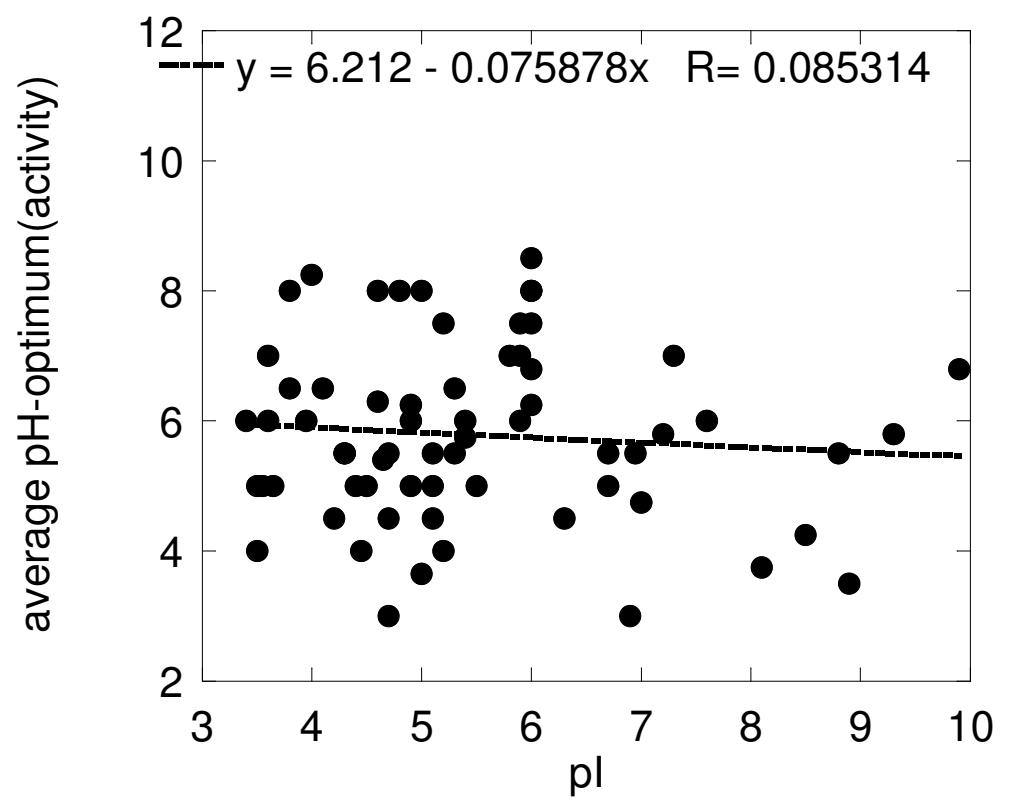


Fig. 3S. Average pH-optimum of activity plotted against the pI.

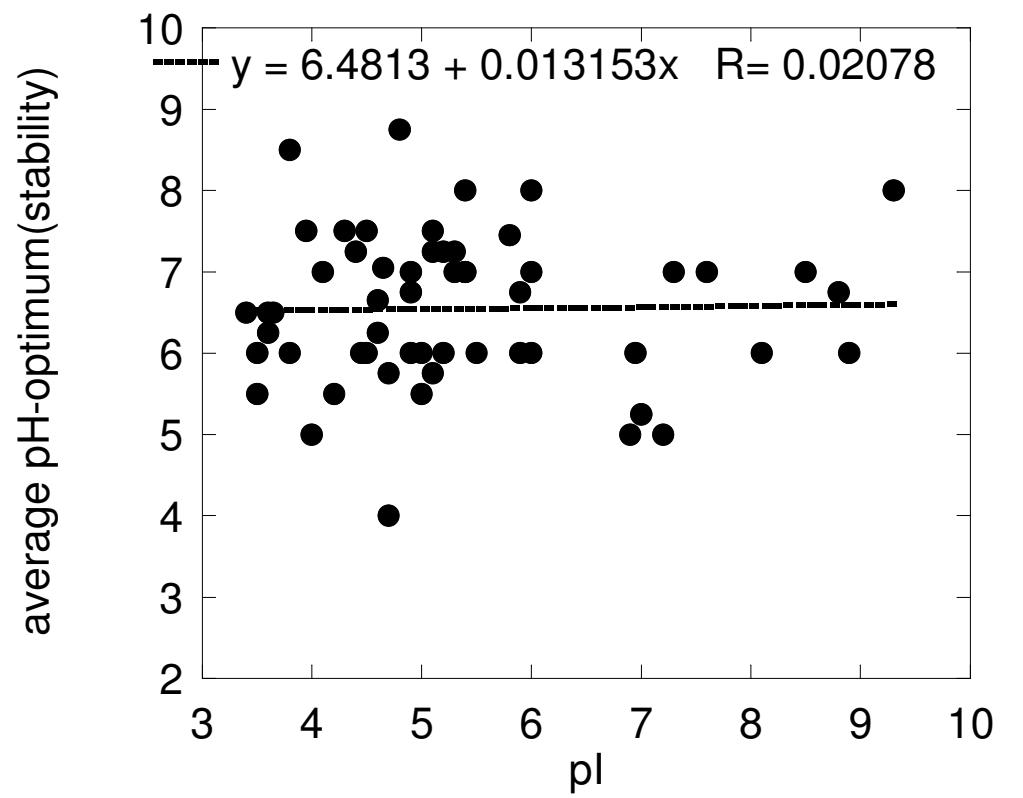


Fig. 4S. Average pH-optimum of stability plotted against the pI.

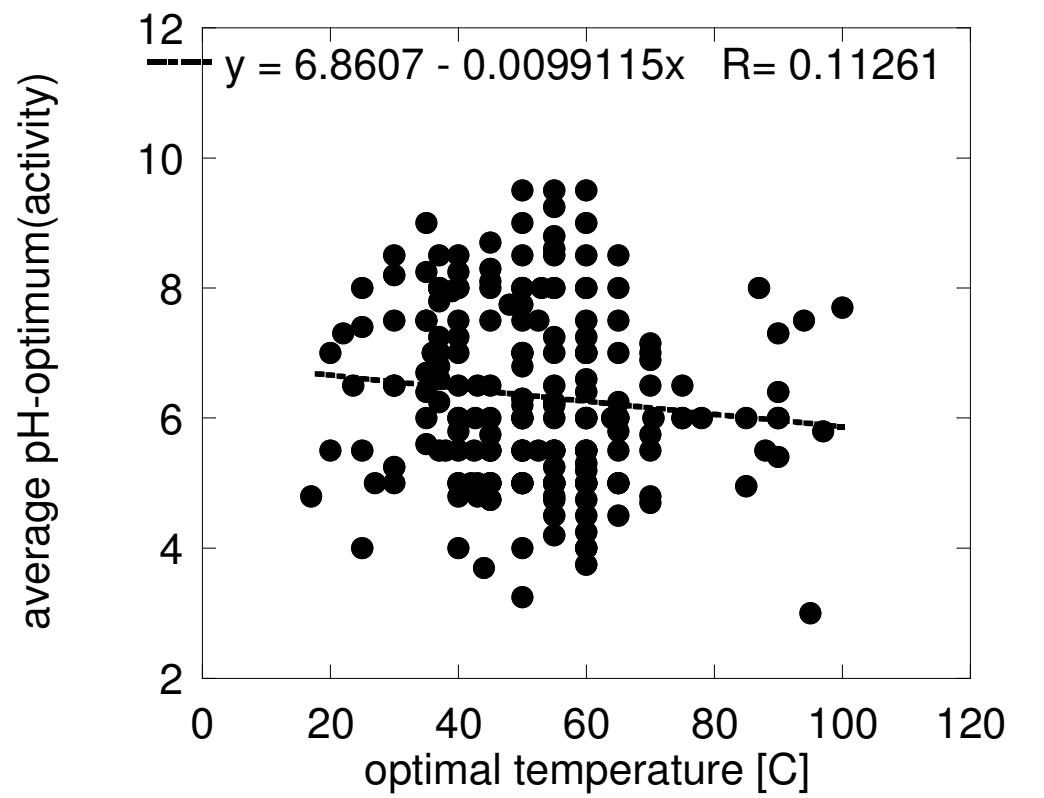


Fig. 5S. Average pH-optimum of activity plotted against the optimal temperature.

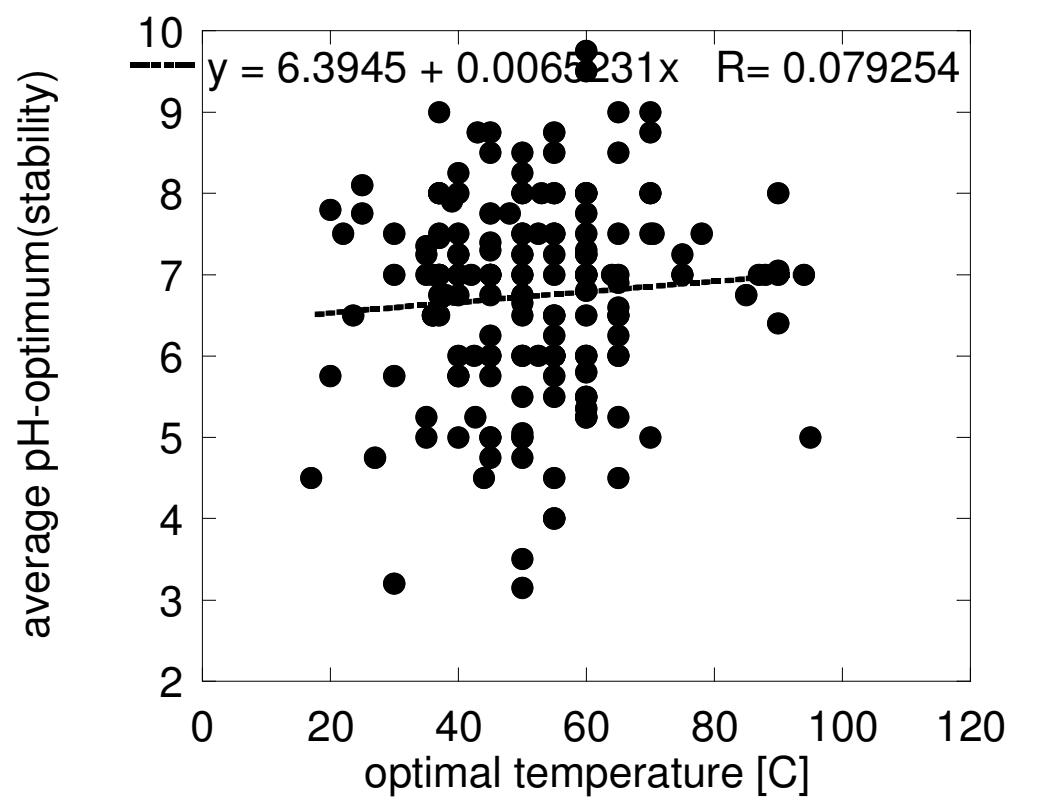


Fig. 6S. Average pH-optimum of stability plotted against optimal temperature